

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):



1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.



2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).



3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).



4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."



5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).



6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).



7. SEE ATTACHED VALIDATION REPORT / INCLUDES CONTACT INFO.
Other: _____

Applicant must provide:

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"



An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification



A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call ~~(703) 308-1123~~

For CRF submission help, call ~~(703) 308-4212~~

For PatentIn software help, call ~~(703) 557-0400~~

Phillip Gambel
PHILLIP GAMBEL, PH.D
PRIMARY EXAMINER

Please return a copy of this notice with your response.

3/10/08

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=25; hr=18; min=3; sec=53; ms=549;]

=====

Reviewer Comments:

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.

Nadler, Lee M.

Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH INCREASED IMMUNOGENICITY AND USES THEREFOR

The above (ii) TITLE OF INVENTION: line exceeds the Sequence Rules' required 72-character limit (this includes white spaces). Please insert a hard return after "WITH" above.

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Per the Sequence Rules, the "INFORMATION FOR SEQ ID NO:" heading is always preceded by a "(2)," regardless of the Sequence ID number.

Please do not number this heading consecutively. Replace the above (3) INFORMATION FOR SEQ ID NO:2: with (2) INFORMATION FOR SEQ ID NO:2:. Please do the same with the subsequent sequences.

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTTAGAGCACA

Please replace the (10) INFORMATION FOR SEQ ID NO:9: with (2) INFORMATION FOR SEQ ID NO:9:. Please insert a space after each group of 10 nucleotides, and insert the cumulative nucleotide total at the right margin. These errors occur in subsequent sequences, too.

Validated By CRFValidator v 1.0.3

Application No: 10767561

Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-17 17:06:18.746
Finished: 2008-01-17 17:06:19.572
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 826 ms
Total Warnings: 0
Total Errors: 66
No. of SeqIDs Defined: 17
Actual SeqID Count: 1

Error code	Error Description
E 200	Mandatory field label missing: in 2_i_C
E 200	Mandatory field label missing: in 2_ii
E 200	Mandatory field label missing: in 2_vi_D
E 200	Mandatory field label missing: in 2_i_C
E 104	Command to process tag does not exist: Tag: 11
E 104	Command to process tag does not exist: Tag: 11_i
E 104	Command to process tag does not exist: Tag: 11_i_A
E 104	Command to process tag does not exist: Tag: 11_i_B
E 104	Command to process tag does not exist: Tag: 11_i_C
E 104	Command to process tag does not exist: Tag: 11_i_D
E 104	Command to process tag does not exist: Tag: 11_ii
E 104	Command to process tag does not exist: Tag: 11_xi
E 104	Command to process tag does not exist: Tag: 12
E 104	Command to process tag does not exist: Tag: 12_i
E 104	Command to process tag does not exist: Tag: 12_i_A
E 104	Command to process tag does not exist: Tag: 12_i_B
E 104	Command to process tag does not exist: Tag: 12_i_C
E 104	Command to process tag does not exist: Tag: 12_i_D
E 104	Command to process tag does not exist: Tag: 12_ii
E 104	Command to process tag does not exist: Tag: 12_xi

Input Set:

Output Set:

Started: 2008-01-17 17:06:18.746
Finished: 2008-01-17 17:06:19.572
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 826 ms
Total Warnings: 0
Total Errors: 66
No. of SeqIDs Defined: 17
Actual SeqID Count: 1

Error code	Error Description
E 104	Command to process tag does not exist: Tag: 12_i
E 104	Command to process tag does not exist: Tag: 12_i_A
E 104	Command to process tag does not exist: Tag: 12_i_B
E 104	Command to process tag does not exist: Tag: 12_i_C This error has occurred more than 20 times, will not be displayed
E 252	Calc# of Seq. differs from actual; 17 seqIds defined; count=1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH INCREASED IMMUNOGENICITY
AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley Hoag
(B) STREET: 155 Seaport Boulevard
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10767561
(B) FILING DATE: 2004-01-28

(vii) PRIOR APPLICATION DATA:

(B) FILING DATE: 28-JAN-2004
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/101,624;
(B) FILING DATE: 26-JUL-1993;
(A) APPLICATION NUMBER: 08/109,393;
(b) FILING DATE: 19-AUG-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Russell, Hathaway P.
(B) REGISTRATION NUMBER: 46,488
(C) REFERENCE/DOCKET NUMBER: WYS-018.04

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT      60
GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC      115
                                     Met Asp Pro
                                     1
CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG      163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
   5                10                15
CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT      211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
  20                25                30                35
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT      259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
          40                45                50
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG      307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
          55                60                65
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG      355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
          70                75                80
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT      403
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
          85                90                95
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA      451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
100                105                110                115
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA      499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
          120                125                130
```

GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
135 140 145	
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
150 155 160	
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	
165 170 175	
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	
180 185 190 195	
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739
Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	
200 205 210	
AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT	787
Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	
215 220 225	
TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA	835
Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	
230 235 240	
GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT	883
Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	
245 250 255	
GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG	931
Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	
260 265 270 275	
CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG	979
Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	
280 285 290	
AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT	1027
Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	
295 300 305	
GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC	1075
Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp	
310 315 320	
AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA	1120
Lys Ser Asp Thr Cys Phe	
325	

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Pro	Gln	Cys	Thr	Met	Gly	Leu	Ser	Asn	Ile	Leu	Phe	Val	Met
1				5					10					15	
Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe
			20					25					30		
Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln
		35					40					45			
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val
	50					55					60				
Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser
65					70					75					80
Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg
				85					90					95	
Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile
			100					105					110		
His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser
		115					120					125			
Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile
	130					135					140				
Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile
145					150					155					160
His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys
				165					170					175	
Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn
		180						185					190		
Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro
	195						200					205			
Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys
	210					215					220				
Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln
225					230					235					240
Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val
				245					250					255	
Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys

260	265	270
Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu		
275	280	285
Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro		
290	295	300
Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser		
305	310	315
		320
Ser Cys Asp Lys Ser Asp Thr Cys Phe		
	325	

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 99..1028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT	60
CCTGTAGACG TGTTCAGAA CTTACGGAAG CACCCACG ATG GAC	100
Met Asp	
1	
CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG	150
Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu	
5 10 15	
CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG	200
Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly	
20 25 30	
ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG	250
Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu	
35 40 45 50	
AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC	300
Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr	
55 60 65	
GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC	350
Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr	
70 75 80	

CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC	
Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His	
85 90 95	
AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA	440
Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys	
100 105 110	
AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG	488
Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu	
115 120 125 130	
TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT	536
Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn	
135 140 145	
GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT	584
Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly	
150 155 160	
CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT	632
His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn	
165 170 175	
GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG	680
Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu	
180 185 190	
TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG	728
Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp	
195 200 205 210	
CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC	776
His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser	
215 220 225	
TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT	824
Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr	
230 235 240	
TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG	872
Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met	
245 250 255	
CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC	920
Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro	
260 265 270	
AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG	968
Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu	
275 280 285 290	
ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA	1016
Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro	
295 300 305	

1069

ATTCTACAGT TGAATAATTA AAGAAC 1151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
180 185 190

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
 195 200 205
 Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
 210 215 220
 Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
 225 230 235 240
 Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
 245 250 255
 Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
 260 265 270
 Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
 275 280 285
 Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
 290 295 300
 Lys Pro Asn Ala Glu
 305

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120
 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240
 TTGCACCTGG GAAGTGCCTT GGTCTTACTT GGTCCAAAT TGTGGCTTT CACTTTTGAC 300

CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
-30 -25

AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
-20 -15 -10

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
-5 1 5 10

GTG GCA AC